

PCT 09

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/09/869,106

DATE: 07/09/2001  
TIME: 10:18:53

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Output Set: N:\CRF3\07092001\I869106.raw

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3 <110> APPLICANT: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)  
 4 POQUET, Isabelle  
 5 GRUSS, Alexandra  
 6 BOLOTINE, Alexandre  
 7 SOROKINE, Alexei  
 9 <120> TITLE OF INVENTION: GRAM-POSITIVE BACTERIA DEPRIVED OF HtrA PROTEASIC  
 10 ACTIVITY, AND THEIR USES  
 12 <130> FILE REFERENCE: 45636-5048-US  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/869,106  
 C--> 15 <141> CURRENT FILING DATE: 2001-06-22  
 17 <150> PRIOR APPLICATION NUMBER: FR98/16462  
 18 <151> PRIOR FILING DATE: 1998-12-24  
 20 <150> PRIOR APPLICATION NUMBER: PCT/FR99/03270  
 21 <151> PRIOR FILING DATE: 1999-12-23  
 23 <160> NUMBER OF SEQ ID NOS: 2  
 25 <170> SOFTWARE: PatentIn Ver. 2.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1740  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Lactococcus lactis  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (230)..(1453)  
 36 <400> SEQUENCE: 1  
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 39 aactttatta aaatatccac ttatcctcat taattttag attatccaca aaaatgtgaa 120  
 41 gaaactatat tagttgatt ttgttacta ttaaggattt attaagttag agtagatata 180  
 43 attacatcat agaaaatgcta caaagattaa taattgaaag gaatttattt atg gca aaa 238  
 44 Met Ala Lys  
 45 1  
 47 gct aat ata gga aaa ttg cta tta aca ggt gtc gtg ggc gga gcc atc 286  
 48 Ala Asn Ile Gly Lys Leu Leu Leu Thr Gly Val Val Gly Gly Ala Ile  
 49 5 10 15  
 51 gca ctt gga gga agt gca atc tat caa agc act aca aat caa tcg gca 334  
 52 Ala Leu Gly Gly Ser Ala Ile Tyr Gln Ser Thr Thr Asn Gln Ser Ala  
 53 20 25 30 35  
 55 aat aat agt cgt tca aat aca act agt aca aag gtt agt aac gtt tcg 382  
 56 Asn Asn Ser Arg Ser Asn Thr Thr Ser Thr Lys Val Ser Asn Val Ser  
 57 40 45 50  
 59 gta aat gtc aat acc gat gtt acc tct gca att gaa aaa gtt tca aat 430  
 60 Val Asn Val Asn Thr Asp Val Thr Ser Ala Ile Glu Lys Val Ser Asn  
 61 55 60 65  
 63 tct gtc gtt tct gtt atg aat tat caa aaa gat aac tca caa agt agt 478  
 64 Ser Val Val Ser Val Met Asn Tyr Gln Lys Asp Asn Ser Gln Ser Ser  
 65 70 75 80  
 67 gac ttc agt tca att ttt ggt gga aat agc ggt tca agt tca tcg act 526  
 68 Asp Phe Ser Ser Ile Phe Gly Gly Asn Ser Gly Ser Ser Ser Ser Thr

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69	85	90	95	
71	gat ggc tta cag ctt tct agt gaa ggc tct ggt gtc atc tac aaa aaa			574
72	Asp Gly Leu Gln Leu Ser Ser Glu Gly Ser Gly Val Ile Tyr Lys Lys			
73	100	105	110	115
75	tct ggt ggt gat gcc tac gtt gta act aac tac cac gtt att gct ggt			622
76	Ser Gly Gly Asp Ala Tyr Val Val Thr Asn Tyr His Val Ile Ala Gly			
77	120	125	130	
79	aat agc tca ctt gat gtt ctg ctt tct ggt gga caa aaa gtc aaa gat			670
80	Asn Ser Ser Leu Asp Val Leu Leu Ser Gly Gly Gln Lys Val Lys Asp			
81	135	140	145	
83	tct gtg gtt ggt tat gat gaa tac aca gac ctt gct gtt ctt aaa atc			718
84	Ser Val Val Gly Tyr Asp Glu Tyr Thr Asp Leu Ala Val Leu Lys Ile			
85	150	155	160	
87	agt tct gaa cat gtc aaa gat gtg gcg aca ttc gct gat tct agt aaa			766
88	Ser Ser Glu His Val Lys Asp Val Ala Thr Phe Ala Asp Ser Ser Lys			
89	165	170	175	
91	tta aca att ggt gaa cct gcc att gcc gtt ggc tca cct tta ggt agt			814
92	Leu Thr Ile Gly Glu Pro Ala Ile Ala Val Gly Ser Pro Leu Gly Ser			
93	180	185	190	195
95	caa ttt gca aac acc gca act gaa gga att tta tct gca aca agc cgt			862
96	Gln Phe Ala Asn Thr Ala Thr Glu Gly Ile Leu Ser Ala Thr Ser Arg			
97	200	205	210	
99	caa gtg act ttg acc caa gaa aat ggt caa aca act aat atc aat gca			910
100	Gln Val Thr Leu Thr Gln Glu Asn Gly Gln Thr Thr Asn Ile Asn Ala			
101	215	220	225	
103	att caa aca gat gct gcc att aac cct ggt aac tct gga ggg gct ttg			958
104	Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly Gly Ala Leu			
105	230	235	240	
107	att aat att gaa gga caa gtt att gga att act caa agt aaa att aca			1006
108	Ile Asn Ile Glu Gly Gln Val Ile Gly Ile Thr Gln Ser Lys Ile Thr			
109	245	250	255	
111	aca act gaa gat ggt tct act tct gtc gaa ggt tta gga ttt gcg att			1054
112	Thr Thr Glu Asp Gly Ser Thr Ser Val Glu Gly Leu Gly Phe Ala Ile			
113	260	265	270	275
115	cct tct aat gat gtc gta aat atc att aat aaa ctt gaa gat gat ggt			1102
116	Pro Ser Asn Asp Val Val Asn Ile Ile Asn Lys Leu Glu Asp Asp Gly			
117	280	285	290	
119	aag att tca cgc cct gct tta ggt atc cga atg gtt gac ctt tca caa			1150
120	Lys Ile Ser Arg Pro Ala Leu Gly Ile Arg Met Val Asp Leu Ser Gln			
121	295	300	305	
123	tta tca aca aat gac agt tct caa ttg aaa tta cta agc agt gta aca			1198
124	Leu Ser Thr Asn Asp Ser Ser Gln Leu Lys Leu Leu Ser Ser Val Thr			
125	310	315	320	
127	ggt ggg gtt gtt tac tcc gtc caa tct gga ctt cct gct gcc tca			1246
128	Gly Gly Val Val Val Tyr Ser Val Gln Ser Gly Leu Pro Ala Ala Ser			
129	325	330	335	
131	gct ggt ttg aaa gct gga gat gta att aca aag gtt ggc gat aca gca			1294
132	Ala Gly Leu Lys Ala Gly Asp Val Ile Thr Lys Val Gly Asp Thr Ala			
133	340	345	350	355

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135 gta acc tct tca aca gac ttg caa agt gct ctt tac tca cac aat atc 1342  
136 Val Thr Ser Ser Thr Asp Leu Gln Ser Ala Leu Tyr Ser His Asn Ile  
137 360 365 370  
139 aat gat aca gta aaa gtt act tat tat cgt gat ggt aaa tca aat aca 1390  
140 Asn Asp Thr Val Lys Val Thr Tyr Tyr Arg Asp Gly Lys Ser Asn Thr  
141 375 380 385  
143 gca gat gtt aaa ctt tct aaa tca acc agt gac tta gaa aca agc agt 1438  
144 Ala Asp Val Lys Leu Ser Lys Ser Thr Ser Asp Leu Glu Thr Ser Ser  
145 390 395 400  
147 cca tct tct tct aat taataactta ataatttaat aaaagtcttc tgtaaataga 1493  
148 Pro Ser Ser Ser Asn  
149 405  
151 aggctttttt catactaaag tctgaaattt ttaaaaataa taaatttcca tttttttttt 1553  
153 attgatttat ggtaaaataa agttaagcat gaaaattta cttaacttag aagccgaaca 1613  
155 attttgagt cattcaggaa ttggtcgtgc aatgaaacat caacaacgcg cccttgattt 1673  
157 aatgggcatt gactggacaa aaaatcctga ggtatgattac gatatcctcc atttaataac 1733  
159 ttatggc 1740  
162 <210> SEQ ID NO: 2  
163 <211> LENGTH: 408  
164 <212> TYPE: PRT  
165 <213> ORGANISM: Lactococcus lactis  
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171 Gly Ala Ile Ala Leu Gly Gly Ser Ala Ile Tyr Gln Ser Thr Thr Asn  
172 20 25 30  
174 Gln Ser Ala Asn Asn Ser Arg Ser Asn Thr Thr Ser Thr Lys Val Ser  
175 35 40 45  
177 Asn Val Ser Val Asn Val Asn Thr Asp Val Thr Ser Ala Ile Glu Lys  
178 50 55 60  
180 Val Ser Asn Ser Val Val Ser Val Met Asn Tyr Gln Lys Asp Asn Ser  
181 65 70 75 80  
183 Gln Ser Ser Asp Phe Ser Ser Ile Phe Gly Gly Asn Ser Gly Ser Ser  
184 85 90 95  
186 Ser Ser Thr Asp Gly Leu Gln Leu Ser Ser Glu Gly Ser Gly Val Ile  
187 100 105 110  
189 Tyr Lys Ser Gly Gly Asp Ala Tyr Val Val Thr Asn Tyr His Val  
190 115 120 125  
192 Ile Ala Gly Asn Ser Ser Leu Asp Val Leu Leu Ser Gly Gly Gln Lys  
193 130 135 140  
195 Val Lys Asp Ser Val Val Gly Tyr Asp Glu Tyr Thr Asp Leu Ala Val  
196 145 150 155 160  
198 Leu Lys Ile Ser Ser Glu His Val Lys Asp Val Ala Thr Phe Ala Asp  
199 165 170 175  
201 Ser Ser Lys Leu Thr Ile Gly Glu Pro Ala Ile Ala Val Gly Ser Pro  
202 180 185 190  
204 Leu Gly Ser Gln Phe Ala Asn Thr Ala Thr Glu Gly Ile Leu Ser Ala  
205 195 200 205  
207 Thr Ser Arg Gln Val Thr Leu Thr Gln Glu Asn Gly Gln Thr Thr Asn

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210	Ile Asn Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly		
211	225	230	235
213	Gly Ala Leu Ile Asn Ile Glu Gly Gln Val Ile Gly Ile Thr Gln Ser		240
214	245	250	255
216	Lys Ile Thr Thr Glu Asp Gly Ser Thr Ser Val Glu Gly Leu Gly		
217	260	265	270
219	Phe Ala Ile Pro Ser Asn Asp Val Val Asn Ile Ile Asn Lys Leu Glu		
220	275	280	285
222	Asp Asp Gly Lys Ile Ser Arg Pro Ala Leu Gly Ile Arg Met Val Asp		
223	290	295	300
225	Leu Ser Gln Leu Ser Thr Asn Asp Ser Ser Gln Leu Lys Leu Leu Ser		
226	305	310	315
228	Ser Val Thr Gly Gly Val Val Val Tyr Ser Val Gln Ser Gly Leu Pro		320
229	325	330	335
231	Ala Ala Ser Ala Gly Leu Lys Ala Gly Asp Val Ile Thr Lys Val Gly		
232	340	345	350
234	Asp Thr Ala Val Thr Ser Ser Thr Asp Leu Gln Ser Ala Leu Tyr Ser		
235	355	360	365
237	His Asn Ile Asn Asp Thr Val Lys Val Thr Tyr Tyr Arg Asp Gly Lys		
238	370	375	380
240	Ser Asn Thr Ala Asp Val Lys Leu Ser Lys Ser Thr Ser Asp Leu Glu		
241	385	390	395
243	Thr Ser Ser Pro Ser Ser Ser Asn		400
244		405	

**VERIFICATION SUMMARY**  
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L:14 M:270 C: Current Application Number differs, Replaced Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date